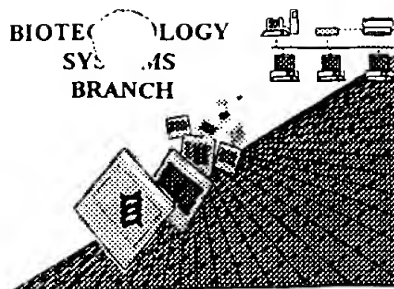


## **RAW SEQUENCE LISTING** **ERROR REPORT**



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/807,949  
Source: PCT 09  
Date Processed by STIC: 5-7-01

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/807,949

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos      The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length      Sequence(s) \_\_\_\_ contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES)      Sequence(s) \_\_\_\_ missing. If intentional, please use the following format for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES)      Sequence(s) \_\_\_\_ missing. If intentional, please use the following format for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 10 ☒ Use of n's or Xaa's (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of "Artificial" (NEW RULES)      Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.  
Valid response is Artificial Sequence.
- 12 ☐ Use of <220>Feature (NEW RULES)      Sequence(s) \_\_\_\_ are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.

PCT

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/807,949

DATE: 05/07/2001

TIME: 14:23:58

Input Set : A:\D-021-51.app

Output Set: N:\CRF3\05072001\I807949.raw

3 <110> APPLICANT: Zavada, Jan  
 4 Pastorekova, Silvia  
 5 Pastorek, Jaromir  
 7 <120> TITLE OF INVENTION: MN Gene and Protein  
 9 <130> FILE REFERENCE: D-0021.5 PCT  
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/807,949  
 C--> 12 <141> CURRENT FILING DATE: 2001-04-19  
 14 <150> PRIOR APPLICATION NUMBER: 09/177,776  
 15 <151> PRIOR FILING DATE: 1998-10-23  
 17 <150> PRIOR APPLICATION NUMBER: 09/178,115  
 18 <151> PRIOR FILING DATE: 1998-10-23  
 20 <160> NUMBER OF SEQ ID NOS: 143  
 22 <170> SOFTWARE: PatentIn Ver. 2.1  
 24 <210> SEQ ID NO: 1  
 25 <211> LENGTH: 1522  
 26 <212> TYPE: DNA  
 27 <213> ORGANISM: HUMAN  
 29 <220> FEATURE:  
 30 <221> NAME/KEY: CDS  
 31 <222> LOCATION: (13)..(1389)  
 33 <220> FEATURE:  
 34 <221> NAME/KEY: mat\_peptide  
 35 <222> LOCATION: (124)..(1389)  
 37 <400> SEQUENCE: 1  
 38 acagtcagcc gc atg gct ccc ctg tgc ccc agc ccc tgg ctc cct ctg ttg 51  
 39 Met Ala Pro Leu Cys Pro Ser Pro Trp Leu Pro Leu Leu  
 40 -35 -30 -25  
 42 atc ccg gcc cct gct cca ggc ctc act gtg caa ctg ctg ctg tca ctg 99  
 43 Ile Pro Ala Pro Ala Pro Gly Leu Thr Val Gln Leu Leu Leu Ser Leu  
 44 -20 -15 -10  
 46 ctg ctt ctg atg cct gtc cat ccc cag agg ttg ccc cgg atg cag gag 147  
 47 Leu Leu Leu Met Pro Val His Pro Gln Arg Leu Pro Arg Met Gln Glu  
 48 -5 -1 1 5  
 50 gat tcc ccc ttg gga gga ggc tct tct ggg gaa gat gac cca ctg ggc 195  
 51 Asp Ser Pro Leu Gly Gly Ser Ser Gly Glu Asp Asp Pro Leu Gly  
 52 10 15 20  
 54 gag gag gat ctg ccc agt gaa gag gat tca ccc aga gag gag gat cca 243  
 55 Glu Glu Asp Leu Pro Ser Glu Glu Asp Ser Pro Arg Glu Glu Asp Pro  
 56 25 30 35 40  
 58 ccc gga gag gag gat cta cct gga gag gag gat cta cct gga gag gag 291  
 59 Pro Gly Glu Glu Asp Leu Pro Gly Glu Asp Leu Pro Gly Glu Glu  
 60 45 50 55  
 62 gat cta cct gaa gtt aag cct aaa tca gaa gaa gag ggc tcc ctg aag 339  
 63 Asp Leu Pro Glu Val Lys Pro Lys Ser Glu Glu Glu Gly Ser Leu Lys  
 64 60 65 70  
 66 tta gag gat cta cct act gtt gag gct cct gga gat cct caa gaa ccc 387  
 67 Leu Glu Asp Leu Pro Thr Val Glu Ala Pro Gly Asp Pro Gln Glu Pro

Does Not Comply  
 Corrected Diskette Needed

pp. 4-5

## RAW SEQUENCE LISTING

DATE: 05/07/2001

PATENT APPLICATION: US/09/807,949

TIME: 14:23:58

Input Set : A:\D-021-51.app

Output Set: N:\CRF3\05072001\I807949.raw

```

68      75      80      85
70 cag aat aat gcc cac agg gac aaa gaa ggg gat gac cag agt cat tgg 435
71 Gln Asn Asn Ala His Arg Asp Lys Glu Gly Asp Asp Gln Ser His Trp
72      90      95      100
74 cgc tat gga ggc gac ccg ccc tgg ccc cgg gtg tcc cca gcc tgc gcg 483
75 Arg Tyr Gly Gly Asp Pro Pro Trp Pro Arg Val Ser Pro Ala Cys Ala
76 105      110      115      120
78 ggc cgc ttc cag tcc ccg gtg gat atc cgc ccc cag ctc gcc gcc ttc 531
79 Gly Arg Phe Gln Ser Pro Val Asp Ile Arg Pro Gln Leu Ala Ala Phe
80      125      130      135
82 tgc ccg gcc ctg cgc ccc ctg gaa ctc ctg ggc ttc cag ctc ccg ccg 579
83 Cys Pro Ala Leu Arg Pro Leu Glu Leu Leu Gly Phe Gln Leu Pro Pro
84      140      145      150
86 ctc cca gaa ctg cgc ctg cgc aac aat ggc cac agt gtg caa ctg acc 627
87 Leu Pro Glu Leu Arg Leu Arg Asn Asn Gly His Ser Val Gln Leu Thr
88      155      160      165
90 ctg cct cct ggg cta gag atg gct ctg ggt ccc ggg cgg gag tac cgg 675
91 Leu Pro Pro Gly Leu Glu Met Ala Leu Gly Pro Gly Arg Glu Tyr Arg
92      170      175      180
94 gct ctg cag ctg cat ctg cac tgg ggg gct gca ggt cgt ccg ggc tgc 723
95 Ala Leu Gln Leu His Leu His Trp Gly Ala Ala Gly Arg Pro Gly Ser
96 185      190      195      200
98 gag cac act gtg gaa ggc cac cgt ttc cct gcc gag atc cac gtg gtt 771
99 Glu His Thr Val Glu Gly His Arg Phe Pro Ala Glu Ile His Val Val
100      205      210      215
102 cac ctc agc acc gcc ttt gcc aga gtt gac gag gcc ttg ggg cgc ccg 819
103 His Leu Ser Thr Ala Phe Ala Arg Val Asp Glu Ala Leu Gly Arg Pro
104      220      225      230
106 gga ggc ctg gcc gtg ttg gcc gcc ttt ctg gag gag ggc ccg gaa gaa 867
107 Gly Gly Leu Ala Val Leu Ala Ala Phe Leu Glu Glu Gly Pro Glu Glu
108      235      240      245
110 aac agt gcc tat gag cag ttg ctg tct cgc ttg gaa gaa atc gct gag 915
111 Asn Ser Ala Tyr Glu Gln Leu Leu Ser Arg Leu Glu Glu Ile Ala Glu
112      250      255      260
114 gaa ggc tca gag act cag gtc cca gga ctg gac ata tct gca ctc ctg 963
115 Glu Gly Ser Glu Thr Gln Val Pro Gly Leu Asp Ile Ser Ala Leu Leu
116 265      270      275      280
118 ccc tct gac ttc agc cgc tac ttc caa tat gag ggg tct ctg act aca 1011
119 Pro Ser Asp Phe Ser Arg Tyr Phe Gln Tyr Glu Gly Ser Leu Thr Thr
120      285      290      295
122 ccg ccc tgt gcc cag ggt gtc atc tgg act gtg ttt aac cag aca gtg 1059
123 Pro Pro Cys Ala Gln Gly Val Ile Trp Thr Val Phe Asn Gln Thr Val
124      300      305      310
126 atg ctg agt gct aag cag ctc cac acc ctc tct gac acc ctg tgg gga 1107
127 Met Leu Ser Ala Lys Gln Leu His Thr Leu Ser Asp Thr Leu Trp Gly
128      315      320      325
130 cct ggt gac tct cgg cta cag ctg aac ttc cga gcg acg cag cct ttg 1155
131 Pro Gly Asp Ser Arg Leu Gln Leu Asn Phe Arg Ala Thr Gln Pro Leu
132      330      335      340

```

## RAW SEQUENCE LISTING

DATE: 05/07/2001

PATENT APPLICATION: US/09/807,949

TIME: 14:23:58

Input Set : A:\D-021-51.app

Output Set: N:\CRF3\05072001\I807949.raw

```

134 aat ggg cga gtg att gag gcc tcc ttc cct gct gga gtg gac agc agt 1203
135 Asn Gly Arg Val Ile Glu Ala Ser Phe Pro Ala Gly Val Asp Ser Ser
136 345 350 355 360
138 cct cgg gct gct gag cca gtc cag ctg aat tcc tgc ctg gct gct ggt 1251
139 Pro Arg Ala Ala Glu Pro Val Gln Leu Asn Ser Cys Leu Ala Ala Gly
140 365 370 375
142 gac atc cta gcc ctg gtt ttt ggc ctc ctt ttt gct gtc acc agc gtc 1299
143 Asp Ile Leu Ala Leu Val Phe Gly Leu Leu Phe Ala Val Thr Ser Val
144 380 385 390
146 gcg ttc ctt gtg cag atg aga agg cag cac aga agg gga acc aaa ggg 1347
147 Ala Phe Leu Val Gln Met Arg Arg Gln His Arg Arg Gly Thr Lys Gly
148 395 400 405
150 ggt gtg agc tac cgc cca gca gag gta gcc gag act gga gcc 1389
151 Gly Val Ser Tyr Arg Pro Ala Glu Val Ala Glu Thr Gly Ala
152 410 415 420
154 tagaggctgg atcttgagaga atgtgagaag ccagccagag gcattctgagg gggagccggt 1449
156 aactgtcctg tctgtctcat tatgccactt ccttttaact gccaaagaaat tttttaaaat 1509
158 aaatatattat aat 1522
161 <210> SEQ ID NO: 2
162 <211> LENGTH: 459
163 <212> TYPE: PRT
164 <213> ORGANISM: HUMAN
166 <400> SEQUENCE: 2
167 Met Ala Pro Leu Cys Pro Ser Pro Trp Leu Pro Leu Leu Ile Pro Ala
168 -35 -30 -25
170 Pro Ala Pro Gly Leu Thr Val Gln Leu Leu Leu Ser Leu Leu Leu Leu
171 -20 -15 -10
173 Met Pro Val His Pro Gln Arg Leu Pro Arg Met Gln Glu Asp Ser Pro
174 -5 -1 1 5 10
176 Leu Gly Gly Gly Ser Ser Gly Glu Asp Asp Pro Leu Gly Glu Glu Asp
177 15 20 25
179 Leu Pro Ser Glu Glu Asp Ser Pro Arg Glu Glu Asp Pro Pro Gly Glu
180 30 35 40
182 Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro
183 45 50 55
185 Glu Val Lys Pro Lys Ser Glu Glu Glu Gly Ser Leu Lys Leu Glu Asp
186 60 65 70 75
188 Leu Pro Thr Val Glu Ala Pro Gly Asp Pro Gln Glu Pro Gln Asn Asn
189 80 85 90
191 Ala His Arg Asp Lys Glu Gly Asp Asp Gln Ser His Trp Arg Tyr Gly
192 95 100 105
194 Gly Asp Pro Pro Trp Pro Arg Val Ser Pro Ala Cys Ala Gly Arg Phe
195 110 115 120
197 Gln Ser Pro Val Asp Ile Arg Pro Gln Leu Ala Ala Phe Cys Pro Ala
198 125 130 135
200 Leu Arg Pro Leu Glu Leu Leu Gly Phe Gln Leu Pro Pro Leu Pro Glu
201 140 145 150 155
203 Leu Arg Leu Arg Asn Asn Gly His Ser Val Gln Leu Thr Leu Pro Pro
204 160 165 170

```

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/807,949

DATE: 05/07/2001

TIME: 14:23:58

Input Set : A:\D-021-51.app

Output Set: N:\CRF3\05072001\I807949.raw

```

206 Gly Leu Glu Met Ala Leu Gly Pro Gly Arg Glu Tyr Arg Ala Leu Gln
207          175          180          185
209 Leu His Leu His Trp Gly Ala Ala Gly Arg Pro Gly Ser Glu His Thr
210          190          195          200
212 Val Glu Gly His Arg Phe Pro Ala Glu Ile His Val Val His Leu Ser
213          205          210          215
215 Thr Ala Phe Ala Arg Val Asp Glu Ala Leu Gly Arg Pro Gly Gly Leu
216 220          225          230          235
218 Ala Val Leu Ala Ala Phe Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala
219          240          245          250
221 Tyr Glu Gln Leu Leu Ser Arg Leu Glu Glu Ile Ala Glu Glu Gly Ser
222          255          260          265
224 Glu Thr Gln Val Pro Gly Leu Asp Ile Ser Ala Leu Leu Pro Ser Asp
225          270          275          280
227 Phe Ser Arg Tyr Phe Gln Tyr Glu Gly Ser Leu Thr Thr Pro Pro Cys
228          285          290          295
230 Ala Gln Gly Val Ile Trp Thr Val Phe Asn Gln Thr Val Met Leu Ser
231 300          305          310          315
233 Ala Lys Gln Leu His Thr Leu Ser Asp Thr Leu Trp Gly Pro Gly Asp
234          320          325          330
236 Ser Arg Leu Gln Leu Asn Phe Arg Ala Thr Gln Pro Leu Asn Gly Arg
237          335          340          345
239 Val Ile Glu Ala Ser Phe Pro Ala Gly Val Asp Ser Ser Pro Arg Ala
240          350          355          360
242 Ala Glu Pro Val Gln Leu Asn Ser Cys Leu Ala Ala Gly Asp Ile Leu
243          365          370          375
245 Ala Leu Val Phe Gly Leu Leu Phe Ala Val Thr Ser Val Ala Phe Leu
246 380          385          390          395
248 Val Gln Met Arg Arg Gln His Arg Arg Gly Thr Lys Gly Gly Val Ser
249          400          405          410
251 Tyr Arg Pro Ala Glu Val Ala Glu Thr Gly Ala
252          415          420

```

256 &lt;210&gt; SEQ ID NO: 3

257 &lt;211&gt; LENGTH: 29

258 &lt;212&gt; TYPE: DNA

259 &lt;213&gt; ORGANISM: HUMAN

261 &lt;400&gt; SEQUENCE: 3

262 cgcccagtggtgtcatcttcc ccagaagag

29

265 &lt;210&gt; SEQ ID NO: 4

266 &lt;211&gt; LENGTH: 19

267 &lt;212&gt; TYPE: DNA

268 &lt;213&gt; ORGANISM: HUMAN

270 &lt;400&gt; SEQUENCE: 4

271 ggaatcctcc tgcattccgg

19

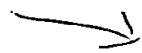
274 &lt;210&gt; SEQ ID NO: 5

275 &lt;211&gt; LENGTH: 10898

276 &lt;212&gt; TYPE: DNA

277 &lt;213&gt; ORGANISM: HUMAN

279 &lt;220&gt; FEATURE:



missing mandatory <220> to <223>  
features to explain the "n" at  
position 1974 in the sequence.

See #10 on the Error Summary Sheet.

Note: This error is indicated elsewhere  
in the sequence listing. Please review  
and correct.

## VERIFICATION SUMMARY

DATE: 05/07/2001

PATENT APPLICATION: US/09/807,949

TIME: 14:23:59

Input Set : A:\D-021-51.app

Output Set: N:\CRF3\05072001\I807949.raw

L:11 M:270 C: Current Application Number differs, Replaced Application Number  
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:316 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5  
L:316 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:512 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9  
L:512 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:688 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:25  
L:688 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25  
L:702 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:26  
L:702 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26  
L:1371 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:58  
L:1371 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58  
L:1804 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:90  
L:1804 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:90  
L:2064 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:110  
L:2064 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:110

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/807,949

DATE: 05/07/2001  
TIME: 14:23:58

Input Set : A:\D-021-51.app  
Output Set : N:\CRF3\05072001\1807949.raw

280 <221> NAME/KEY: gene  
281 <222> LOCATION: (1)..(10898)  
283 <400> SEQUENCE: 5

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284 ggatcctgtt gactcgtgac cttacccccca accctgtgtct ctctgaaaca tgagctgtgt 60
285 ccactcaggg ttaaattgat taagggcggt gcaagatgtg ctttgtaaag cagatgcttg 120
286 aaggcagcat gctcgttaag agtcatcacc aatccctaatt ctcaagtaat cagggacaca 180
287 aacactgcgg aaggccgcag ggtccctctgc ctaggaaaac cagagacctt tgttcacttg 240
288 tttatctgac cttccctcca ctattgtcca tgaccctgcc aaatccccct ctgtgagaaa 300
289 caccacaaga ttatcaataa aaaaataaat ttaaaaaaaa aatacaaaaa aaaaaaaaaa 360
290 aaaaaaaaaa gacttacgaa tagttattga taaatgaata gctattggta aagccaagta 420
291 aatgatcata ttcaaaacca gacggccatc atcacagctc aagtctacct gatttgatct 480
292 ctttatcatt gtcattcttt ggattcacta gattagtcac catcctcaaa attctcccc 540
293 aagttctaatt tacgttccaa acatttaggg gttacatgaa gcttgaacct actacctct 600
294 ttgcttttga gccatgagtt gtaggaatga tgagtttaca ccttacatgc tggggattaa 660
295 ttttaacttt acctctaagt cagttgggta cacccttggt tatttttgta gctaattttg 720
296 tagttaatgg atgcactgtg aatcttgcta tgatagtttt cctccacact ttgccactag 780
297 gggtaggtag gtactcagtt ttcagtaatt gcttacctaa gaccctaagc cctattttct 840
298 ttgtactggc ctttatctgt aatatgggca tattaatac aatataattt ttggagtttt 900
299 tttgtttgtt tgttttgttg tttttttgag acggagtctt gcatctgtca tgcccaggct 960
300 ggagtagcag tgggtgccatc tgggtcact gcaagctcca cctcccgagt tcacgccatt 1020
301 ttccctgctc agcctcccca gtagctggga ctacaggcgc ccgccaccat gcccggttaa 1080
302 ttttttggat ttttggtaga gacggggttt caccgtgtta gccagaatgg tctcgatctc 1140
303 ctgacttcgt gatccacccg cctcggcctc ccaaagttct gggattacag gtgtgagcca 1200
304 ccgcacctgg ccaatttttt gagtctttta aagtaaaaat atgtcttgta agctggtaac 1260
305 tatggtacat ttccctttat taatgtggtg ctgacggcca tataggttct tttgagtttg 1320
306 gcatgcata gctacttttt gcagtccctt cattacattt ttctctcttc atttgaagag 1380
307 catgttatat cttttagctt cacttggttt aaaaagttct ctcatagcc taacacagt 1440
308 tcattgttgg taccacttgg atcataagtg gaaaaacagt caagaaattg cacagtaata 1500
309 cttgttttga agagggatga ttccaggtgaa tctgacacta agaaactccc ctacctgagg 1560
310 totgagatc ctctgacatt gctgtatata ggcttttctt ttgacagcct gtgactgcgg 1620
311 actatttttc ttaagcaaga tatgctaaag tttgtgagc ctttttccag agagaggtct 1680
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315 gggtcataat ctcaattctg tcagaattgg tacaagaaat agctgctatg tttcttgaca 1920
W--> 316 ttccacttgg taggaaataa gaatgtgaaa ctcttcagtt ggtgtgtgtc ccttttttt 1980
317 ttgcaatttc cttcttactg tgtaaaaaaa aagtatgac ttgctctgag aggtgaggca 2040
318 ttcttaatac tgatctttta agatcaataa tataatcctt tcaaggatta tgtctttatt 2100
319 ataataaaga taatttgtct ttaacagaat caataatata atccctaaa ggattataat 2160
320 tttgctgggc gcagtggctc acacctgtaa tcccagcact ttgggtggcc aaggtggaag 2220
321 gatcaaatg gctacttct atattatctt ctaaaagcaga attcatctct cttccctcaa 2280
322 tatgatgata ttgacagggt ttgcccctac tcaatagatt gtgagctcct gctcagggca 2340
323 ggtagcgttt tttgtttttg tttttgtttt tcttttttga gacagggtct tgctctgtca 2400
324 cccaggccag agtgcaatgg tacagtctca gctcactgca gcctcaaccg cctcggtcca 2460
325 aaccatcatc caatttcagc ctctgagta gctgggacta caggcacatg ccattacacc 2520
326 tggctaattt ttttgtattt ctagtagaga cagggtttgg ccatgttgcc cgggctggtc 2580
327 tcgaactcct ggactcaagc aatccaccca cctcagcctc ccaaaatgag ggaccgtgtc 2640
328 ttattcattt ccatgtccct agtcocatag ccagtgtgg acctatggta gtactaaata 2700
329 aatatttggt gaatgcaata gtaaatagca tttcagggag caagaactag attaacaag 2760

```

→ "n" at  
position 1974  
see previous  
page.

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.